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Database :
                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
SPTREMBL_15:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
7: sp_mhc:*
10: sp_plant:*
11: sp_rodent:
12: sp_vertebr
13: sp_vertebr
14: sp_unclass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            March 1, 2001, 16:09:05; Search time 299.73 Seconds (without alignments) 24.636 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-331-631A-1_COPY_186_248
355
1 KRDPQQREYEDCRRRCEQQE.....MMNPQRGGSGRYEEGEEEQS 63
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                             374700 seqs, 117207915 residues
                                                                                                               : sp_archea:*
: sp_bacteria:*
: sp_fungi:*
: sp_human:*
: sp_invertebrate:*
: sp_mammal:*
: sp_mhc:*
              sp_phage:*
): sp_plant:*
: sp_rodent:*
: sp_virus:*
: sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                      sp_organelle:*
 sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	œ	7	6	ر ت	4	ω	2	1		Result
79	79	79	79	79.5	80.5	81.5	. 81.5	82	82	86	87	92	112	120	125.5	320	332	355	OCOL 6	
22.3	22.3	22.3	22.3	22.4	22.7	23.0	23.0	23.1	23.1	24.2	24.5	25.9	31.5	33.8	35.4	90.1	93.5	100.0	HO COL	Query
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Q9 J M 92	Q9P2R8	Q9W4J3	P91419	081254	Q9S709	081261	081260	Q9VJJ9	8FFA60	Q24754	Q9NUA2	Q9ZWI3	Q03678	Q43358	Q9SEW4	Q9SPL3	Q9SPL4	Q9SPL5		3
Q9jm92 mus musculu	Q9p2r8 homo sapien	Q9w4j3 drosophila	P91419 caenorhabdi	O81254 zea mays su	Q9s709 arabidopsis	O81261 tripsacum d	O81260 tripsacum d	Q9vjj9 drosophila	Q9vjj8 drosophila	Q24754 drosophila	Q9nua2 homo sapien	Q9zwi3 cucurbita m	Q03678 hordeum vul	<u>-</u>	. Q9sew4 juglans reg	Q9spl3 macadamia i	Q9spl4 macadamia i	Q9spl5 macadamia i	Description	

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	20.8	20.8	20.8	20.8	20.8	20.8	21.1	21.1	21.1	21.3	21.3	21.3	21.3	21.4	21.4	21.4	21.4	21.4	21.4	21.5	21.7	21.7	21.8	22.1	22.3	22.3
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		060983 dictyosteli	O60424 homo sapien	zea	Q9sbe5 zea luxuria	O81258 zea luxuria	Q23901 dictyosteli	Q9ztp0 oryza sativ			076940 drosophila		O18118 caenorhabdi	Q9u4i2 drosophila	Q9u9s7 dictyosteli	Q9un21 homo sapien	Q23847 dictyosteli	Q9sbe6 zea mays su	081251 zea mays su	040947 kaposi's sa	Q9kmz5 vibrio chol	Q9vfn6 drosophila	Q9vd46 drosophila	Q9vz60 drosophila	Q9jm52 mus musc.،	Q9p1x1 homo sapien

ALIGNMENTS

DR HSSP; P02853; 2PHL. DR HSSP; P02853; 2PHL. DR INTERPRO; IPR001113; DR INTERPRO; IPR001113; SQ SEQUENCE 666 AA; 78217 MW; C752B884B2DF0224 CRC64; SQ SEQUENCE 666 AA; 78217 MW; C752B884B2DF0224 CRC64; Query Match Best Local Similarity 100.0%; Pred. No. 4.7e-35; Best Local Similarity 100.0%; Pred. No. 4.7e-35; Matches 63; Conservative 0; Mismatches 0; Indels 0; G Oy 1 KRDPQOREYEDCRRRCEBQEPRQOHQCOLRCREQQROHGRGGDMMNPQRGGSGRYEBGEE DB 186 KRDPQOREYEDCRRRCEBQEPRQOHQCOLRCREQQROHGRGGDMMNPQRGGSGRYEBGEE DB 186 KRDPQOREYEDCRRRCEBQEPRQOHQCOLRCREQQROHGRGGDMMNPQRGGSGRYEBGEE
Plant J. U:0'-0'(1999). EMBL; AEF161883; AAD54244.1; HSSP; P02853; 2PHL. INTERPRO; IPRO01113; PFAM; PF00546; Seedstore_7s; 1. SEQUENCE 666 AA; 78217 MW; SEQUENCE 666 AA; 100.0%; Secury Match Best Local Similarity 100.0%; PMatches 63; Conservative 0;
Plant J. U:O'U(1999). EMBL; AE161883; AAD54244.1; HSSP; P02853; 2PHL. INTERPRO; IPRO01113; PFAM; PF00546; Seedstore_7s; 1. SEQUENCE 666 AA; 78217 MW;
2
SEQUENTISSUE TISSUE Marcus "A fan globul
DT 01-MAY-2000 (TrEMBLrel. 13, Created) DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) DT 01-CT-2000 (TrEMBLrel. 15, Last annotation update) DE VICILIN PRECURSOR.
SPL
PRT; reate ast se ast a ast ar yoph; proph; pridee integ

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Matches 58
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Best Local
                                                                   Matches
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"A family of antimicrobial pept
globulin protein in Macadamia i
Plant J. 0:0-0(1999).
EMBL; AF161884; AAD54245.1; -.
HSSP; P02853; 2PHL.
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Q9SPL4;
01-MAY-2000
01-MAY-2000
01-OCT-2000
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01-MAY-2000
01-MAY-2000
01-OCT-2000
                                                                                                                                              PFAM; PFC
NON_TER
SEQUENCE
                                                                                                                                                                                                              J. Green J.L., Manners J. globulin protein in Macadamia integrifolia."; Plant J. 0:0-0(1999).

EMBL; AF161885; AAD54246 1
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Magnoliophyta; eudicotyledons; Proteaceae;
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Magnoliophyta; eudicotyledons;
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TISSUE-NUT KERNEL;
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                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=60698;
                                                                                                                                                                                               [NTERPRO;
   145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246
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nes 56; Conser
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PF00546; Seedstor
NCE 666 AA; 782
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(TrEMBLrel. 13, Last sequence up)
(TrEMBLrel. 15, Last annotation)
                                                                   Conservative
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AA; 78243 MW;
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Last annotation updat
                                                                   4;
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No. 7
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Matches 28
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Q43358; O1-NOV-1996 (TrEMBLrel. C
01-NOV-1996 (TrEMBLrel. C
01-OCT-2000 (TrEMBLrel. C
"Comparison of the structure and nucleotide sequences of vicilin genes of cocoa and cotton raise questions about vicilin evolution."; plant Mol. Biol. 18:1173-1170(1992). EMBL; X62625; CAA44493.1; -. EMBL; X62626; CAA44494.1; -. EMBL; X62626; CAA44494.1; -.
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Q9SEW4;
Q9SEW4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-QCT-2000 (TrEMBLrel. 15, Last annotation update)
VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
                                                                                                 MEDLINE=92288309; PubMed=1600151; McHenry L., Fritz P.J.;
                                                                                                                                                                                               Theobroma cacao (Cacao).
Eukaryota; Viridiplantae; Embr.
Magnoliophyta; eudicotyledons;
Malvales; Malvaceae; Theobroma
                                                                                                                                                                                                                                                                CSV
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Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari
"Identification and cloning of a cDNA encoding a vicilin-like
Jug r 2, from English walnut kernel (Juglans regia): a major f
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Magnollophyta; eudicotyledons; core eu
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                                                                                                                                 TISSUE=LEAVES;
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                                                                                                                                                                              NCBI_TaxID=3641;
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28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.48;
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01,
15,
                                                                                                                                                                                                                             Embryophyta;
                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Pred. No. 2.
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Mismatches
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eudicots; Rosidae; eurosids II;
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nes 17;
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                                                                                                                                                                                                              Rosidae;
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Q9ZWI3
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Matches 24
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Best Local :
 Q9ZWI3;
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01-NOV-1996
01-OCT-2000
                                                                                                                                                                                                                                                                                         BEG1 OR GBL1.
Hordeum vulgare (Barley), a
Eukaryota; Viridiplantae; I
Magnoliophyta; Liliopsida;
                                                                                                                                                                                                       PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
PRODOM; PD081059; -; 1.
                                                                                                                                                                                                                                    MENDEL; P02853; 2PHL.
MENDEL; 8553; HOTVU;1188;8553.
INTERPRO; IPR000901; -
INTERPRO; IPR001113; -
                                                                                                                                                                                                                                                                           EMBL; M64372; AAA32936.1;
EMBL; M81719; AAA34269.1;
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                            PFAM; PF00546; Seedstore_7s;
                                                                                                                                                                                                                                                                                                                           MEDLINE=93287988; PubMed=8510647; Heck G.R., Chamberlain A.C., Ho T
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4513,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q03678;
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INTERPRO; IPRO01113; -.
PFAM; PF00546; Seedstore_7s; 1.
                                                          102 RHGEGEREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 ERDPRO-QYEQCQRRCESEATEERREQEQCEQRCEREYKEQQRQQEE--ELQRQYQQCQGR
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                                                                                                                                                                                     storage protein.
ENCE 637 AA; 72252 MW;
                                                                            RYEEGEEEQ 62
                                                                                                QQCVQRCRQERPRYSHARCVQECRDDQQQHGRHEQEEEQGRGRGWHGEGEREEEHGRGRG
                                                                                                                 EDCRRRCEQQEPRQQH-QCQLRCREQQRQHGRGGDMMNPQRG------
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29; Conserv
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24; Conser
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25
525 AA;
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          PRELIMINARY;
                                                                                                                                       Conservative
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01, Last sequence update)
15, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                        and Triticum aestivum (Wheat).
Embryophyta; Tracheophyta; Spermatophyta;
; Poales; Poaceae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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Pred. No. 9.1e-07;
3; Mismatches 17;
                                                                                                                                     Score 112; DB 1
Pred. No. 1e-05;
8; Mismatches
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          PRT;
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RESULT
Q9NUA2
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Best Local :
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Best Local
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J. Biol. Chem. 274:2563-2570(1999).
EMBL; AB019195; BAA34056.1;
INTERPRO; IPR001113;
INTERPRO; IPR001113;
PFAM; PF00546; Seedstore_7s; 1.
PRODOM; PD081059; -; 1
Secures of the functional proteins of the functional processing enzyme.";
                                                                                                                                                                                                                                                                                                              Q9NUA2;
Q9NUA2;
01-OCT-2000
                                                                                                           Receptor.
NON_TER
SEQUENCE
                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DJ80804.1 (ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cucurbita maxima (Pumpkin) (Winter squash).
Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; endicotyledons; core eudicots;
Cucurbitales; Cucurbitaceae; Cucurbita.
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                                                                                                                                                                                     SEQUENCE FROM N.A.
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MEDLINE=99107919; PubMed=9891029;
                                                                                                                                                 EMBL; AL049564;
                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                             (FRAGMENT).
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58 QQQQQQQQQQQQQQQQQQQQTSPRQQQQQQGEDGSPQAHRRGPTGYLVLDEEQQ 115
                        5 QQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQ
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                                                 l Similarity
19; Conser
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                                                                                                                                                              (APR-2000)
                                                                                                             539 AA;
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(TrEMBLrel. 10, Last sequence update)
(TremBLrel. 15, Last annotation updat
                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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55444 MW;
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                                                                                                                                                                                                                                    Chordata;
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                                                           24.5%;
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                                                 15;
                                                                                                                                                 EMBL/GenBank/DDBJ
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Pred. No. 0.0033;
Pred. No. 23;
                                                          Score 87; L
Pred. No. 0.
                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                              AB493953B89D869F
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                                                 Mismatches
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01-MAY-2000
01-MAY-2000
01-JUN-2000
CG4668 PROTE
CG4668.
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01-NOV-1996
01-OCT-2000
                             MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Newfeld S.J., Smoller D.A.
"Interspecific comparison
mastermind.";
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NCBI_TaxID=7244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94111143; PubMed=8283480;
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    Doyle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa; Arthropoda; Tracheata; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               eoptera; Endopterygota; Diptera; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38:637-641(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32:415-420(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smoller D.A., Yedvobnick B comparison of the unusual
С.,
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E.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
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Helt G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1655
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
A Liu X., Mattei B., McIntosh T.C., McLeod M.P., Lilang Y., Lin X.,
A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Spier E., Sprädling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., wu D., Yang S., Yao Q.A.,
A Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
The genome sequence of Drosophila melanogaster.";
EMBL, AE00362; AAF53547.1;
FMFLPBDD., TEDRO17772. CC4668.
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Best Local :
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Q9VJJ9;
01-MAY-2000
01-MAY-2000
01-JUN-2000
CG4668 PROTE
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Fosler C.,
Glodek A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ballew R.M., Basu A., Baxenuaru.... Bhandari D., Bolsnakov Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bottier P., Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brokstein P., Center A., Chr. Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chr. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P. Cherry J.M., Cawley S., Deng Z., Mays A.D., Dew I., Dietz C., Davies B., Delcher A., Deng Z., Mays A.D., Duw D. B.C.
MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J. Adams M.D., Scherer S.E., Li P.W., Hoskins R.A., Galle George R.A., Lewis S.E., Richards S., Ashburner M., Henderso Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.
                                                                                                                                                                                                Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                           CG4668
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PRINTS; PR00014; FNTYPEIII.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
                                                                                                    STRAIN-BERKELEY;
                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                              Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                     Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                              PROTEIN.
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, Evangelista C.C., Ferraz C., Ferriera S., Fleischmann
Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                  Neoptera;
                                                                                                                                                                                                                   melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                              ) (TrEMBLrel. 13,
) (TrEMBLrel. 13,
) (TrEMBLrel. 14,
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                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.1%;
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                                                                                                                                                                                                Endopterygota;
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                                                                                                                                                                            erygota; Diptera;
Drosophila.
                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
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Pred. No. 0.08
6; Mismatches
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.082;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1312;
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                       Henderson
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G.,
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mcrkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Morkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mcrkulov G., Milshina N.V., Mobarry L., Muzny D.M., Nelson D.L.,
RA Morkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mcrkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Morkulov G., Nilson K., Nikon K., Nusskern D.R., Pacleb J.M.,
RA Merkulov G., Nilson K., Nikon K., Nuszkern D.R., Pacleb J.M.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nikon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Wang X.,
RA Williams S.M., Woodage T., Worler E., Wang A., H., Wang X.,
RA Williams S.M., Woodage T., Worler E., Wang S., Yao Q.A.,
RA Williams S.M., Woodage T., Kohan M., Zhang G., Zhao Q., Zheng L.,
RA J., Yeh R., F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Glibbs R.A., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 36.2
                                                                                                                                                                                                                                                         O81260;
01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
            "Speciation and domestication in maize "Speciation and domestication in maize evidence from the Globulin-1 gene."; Genetics 0:0-0(1998).

EMBL; AF064234; AAC31477.1; -.
                                                                                                                                                      Tripsacum dactyloides (Gama grass).
Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; Liliopsida; Poales; Poac
NCBI_TaxID=4563;
                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                          GLOBULIN-1 (FRAGMENT).
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FLYBASE;
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Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00014; FNTYPEIII.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                              217 RRLPQQHQGQAHQ----VAQQQQSQARNGNPQHPQRAGSSVGGASSVGTSEDGEDNSS
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E
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nce 287:2185-2195(2000).
; AE003652; AAF53546.1; -.
ASE; FBGn0032592; CG4668.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.C., Rogers
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                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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15,
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6;
                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                              Poaceae;
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                                                                         its wild relatives:
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                                                                                                                                                                              Tripsacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1323;
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                                                                                                                                                                                                                                                         Q9S709;
Q9S709;
01-MAY-2000
01-MAY-2000
01-JUN-2000
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T17H3.14.
                        Chao Q., Brooks S., Buehler E., Shinn P., Altafi H., Bei Q., Chi
                                                                   SEQUENCE
                                                                                                                                Magnoliophyta; eudicotyledons;
Brassicales; Brassicaceae; Arab
                                                                                                                                                                          Arabidopsis thaliana (Mou: Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLOBULIN-1 (FRAGMENT).
Tripsacum dactyloides (Gama grass).
Eukaryota; Viridiplantae; Embryophyta;
                                                                                                             NCBI_TaxID=3702;
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NON_TER 246 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR001113;
PFAM; PF00546; Seedst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF064235; AAC31478.1; -. HSSP; P50477; ICAU. MENDEL; 31903; Trida;1188;31903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             evidence from the Globulin-1
Genetics 0:0-0(1998).
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NON_TER 242 242
SEQUENCE 242 AA; 27810 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 CRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQR---GGSGRYEEGEEEQ
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      Α.,
                                                                                                                                              (Mouse-ear cress).
ntae; Embryophyta; Tracheophyta; Spermatophyta;
ntae; Embryophyta; Tracheophyta; Rosidae; eurosids II;
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35.2%;
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13,
      Hansen
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E., Johnson-Hopson C.
Chin C., Chiou J., C
en N., Howng B., Koo
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Pred. No. 0.02
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Pred. No. 0
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Poaceae; Tripsacum.
                                                                                                                                                                                                                                                                                                                                            296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
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                     Choi
                   ., Khan S., Kim
Choi E., Conn L.
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RESULT 15
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DR HSSP;
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DR INTERP
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Best Local Similarity
Matches 22; Conserv
                              Query Match
Best Local Similarity
                                                                                                                                                      evidence from the Globulin-1 gene.";
Genetics 0:0-0(1998).
EMBL; AP064222; AAC31465.1; -.
HSSP; P50477; ICAU.
HSSP; P50477; ICAU.
INTERPRO; IPR000901; -.
INTERPRO; IPR001113; -.
INTERPRO; IPR001113;
Matches
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01.NOV-1998 (TrEMBLrel. 08, Created)
01.NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Lee J.M., Liu A., Li J., Gonzalez A., Liu K., Vaysberg M., Sakano H.,
Chin C., Howng B., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.,
Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome 1 BAC T1/Ha Sequence.";
"Arabidopsis thaliana chromosome 1 BAC T1/Ha Sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays subsp. parviglumis.
Eukaryota; Viridiplantae; Embryophyta; Tracheoph
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
NCBI_TaxID-76912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AC012375; AAF24943.1; -. EMBL; AC005916; AAD46002.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLOBULIN-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         081254
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INTERPRO; IPR000571; -.
PFAM; PF00076; rrm; 1.
PFAM; PF00642; zf-CCCH; 2.
SEQUENCE 296 AA; 34572 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hilton H., Gaut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic sequence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Speciation and domestication in maize and its wild relatives:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 RRDPSHREFSHRDRDREFYRHGSGKRSSERSERQERDGSRGRRQASPKRGGSPGGGREGS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 EEQ 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EER 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B.S.;
                                                                                                                                           236
27050 MW; 36A7D94C52l3F206 CRC64;
                                  22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana BAC T22C5 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 80.5; DB. Pred. No. 0.032; 7; Mismatches
   æ
Score 79.5; DB 10;
Pred. No. 0.034;
8; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F284D29BF68445BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                DB 10;
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3.
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                                                                Length 236;
      Indels
      5.
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      Gaps
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Search completed: March 1, 2001, 16:09:07 Job time: 1551 sec